

SEQUENCE LISTING

<110> Cismowski, Mary

Duzic, Emir

<120> AGS Proteins and Nucleic Acid Molecules and Uses Therefor

<130> 60388-A-PCT-US

<140> 09/709,103

<141> 2000-11-08

<160> 73

<170> PatentIn version 3.1

<210> 1

<211> 846

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)..(843)

<223>

<400> 1

atg	aaa	ctg	gcc	gcg	atg	atc	aag	aag	atg	tgc	ccg	agc	gac	tcg	gag	48
Met	Lys	Leu	Ala	Ala	Met	Ile	Lys	Lys	Met	Cys	Pro	Ser	Asp	Ser	Glu	
1				5					10					15		

ctg	agt	atc	ccg	gcc	aag	aac	tgc	tat	cgc	atg	gtc	atc	ctc	ggc	tcg	96
Leu	Ser	Ile	Pro	Ala	Lys	Asn	Cys	Tyr	Arg	Met	Val	Ile	Leu	Gly	Ser	
			20					25						30		

tcc aag gtg ggc aag acg gcc atc gtg tcg cgc ttc ctc acc ggc cgc	144
Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg	
35 40 45	
ttc gag gac gcc tac acg cct acc atc gag gac ttc cac cgc aag ttc	192
Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe	
50 55 60	
tac tcc atc cgc ggc gag gtc tac cag ctc gac atc ctc gac acg tcc	240
Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser	
65 70 75 80	
ggc aac cac ccg ttc ccc gcc atg cgg cgc ctc tcc atc ctc aca gga	288
Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly	
85 90 95	
gac gtt ttc atc ctg gtg ttc agt ctg gac aac cgc gac tcc ttc gag	336
Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu	
100 105 110	
gag gtg cag cgg ctc agg cag cag atc ctc gac acc aag tct tgc ctc	384
Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu	
115 120 125	
aag aac aaa acc aag gag aac gtg gac gtg ccc ctg gtc atc tgc ggc	432
Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly	
130 135 140	
aac aag ggt gac cgc gac ttc tac cgc gag gtg gac cag cgc gag atc	480
Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile	
145 150 155 160	
gag cag ctg gtg ggc gac gac ccc cag cgc tgc gcc tac ttc gag atc	528
Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile	
165 170 175	
tcg gcc aag aag aac agc agc ctg gac cag atg ttc cgc gcg ctc ttc	576
Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe	
180 185 190	
gcc atg gcc aag ctg ccc agc gag atg agc cca gac ctg cac cgc aag	624
Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys	
195 200 205	
gtc tcg gtg cag tac tgc gac gtg ctg cac aag aag gcg ctg cgg aac	672
Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn	
210 215 220	
aag aag ctg ctg cgg gcc ggc agc ggc ggc ggc ggc ggc gac ccg ggc	720
Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Gly Asp Pro Gly	
225 230 235 240	
gac gcc ttt ggc atc gtg gca ccc ttc gcg cgc cgg ccc agc gta cac	768
Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His	
245 250 255	
agc gac ctc atg tac atc cgc gag aag gcc agc gcc ggc agc cag gcc	816
Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala	
260 265 270	

aag gac aag gag cgc tgc gtc atc agc tag
 Lys Asp Lys Glu Arg Cys Val Ile Ser
 275 280

846

<210> 2

<211> 281

<212> PRT

<213> Homo Sapien

<400> 2

Met Lys Leu Ala Ala Met Ile Lys Lys Met Cys Pro Ser Asp Ser Glu
 1 5 10 15

Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
 20 25 30

Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
 35 40 45

Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
 50 55 60

Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
 65 70 75 80

Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
 85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
 100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
 115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
 130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
 145 150 155 160

Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
 165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
 180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
 195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
 210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Gly Asp Pro Gly
 225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
 245 250 255

Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
 260 265 270

Lys Asp Lys Glu Arg Cys Val Ile Ser
 275 280

<210> 3

<211> 1801

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (154)...(996)

<223>

<400> 3
 ggaattccga gcggagccgg agccccaagc ccgagccgcg cccagcccga gcagagccct 60

ccagccgctc accccgcgtg ccaccccagc gaccctcagc cgctctctgc ccttctctcg 120

gccccgcgcc cgccctcgcg gccctctg cca atg aaa ctg gcc gcg atg atc 174
 Met Lys Leu Ala Ala Met Ile
 1 5

aag aag atg tgc ccg agc gac tcg gag ctg agt atc ccg gcc aag aac 222
 Lys Lys Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn
 10 15 20

tgc tat cgc atg gtc atc ctc ggc tcg tcc aag gtg ggc aag acg gcc	270
Cys Tyr Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala	
25 30 35	
atc gtg tcg cgc ttc ctc acc ggc cgc ttc gag gac gcc tac acg cct	318
Ile Val Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Pro	
40 45 50 55	
acc atc gag gac ttc cac cgc aag ttc tac tcc atc cgc ggc gag gtc	366
Thr Ile Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val	
60 65 70	
tac cag ctc gac atc ctc gac acg tcc ggc aac cac ccg ttc ccc gcc	414
Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala	
75 80 85	
atg cgg cgc ctc tcc atc ctc aca gga gac gtt ttc atc ctg gtg ttc	462
Met Arg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe	
90 95 100	
agt ctg gac aac cgc gac tcc ttc gag gag gtg cag cgg ctc agg cag	510
Ser Leu Asp Asn Arg Asp Ser Phe Glu Glu Val Gln Arg Leu Arg Gln	
105 110 115	
cag atc ctc gac acc aag tct tgc ctc aag aac aaa acc aag gag aac	558
Gln Ile Leu Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn	
120 125 130 135	
gtg gac gtg ccc ctg gtc atc tgc ggc aac aag ggt gac cgc gac ttc	606
Val Asp Val Pro Leu Val Ile Cys Gly Asn Lys Gly Asp Arg Asp Phe	
140 145 150	
tac cgc gag gtg gac cag cgc gag atc gag cag ctg gtg ggc gac gac	654
Tyr Arg Glu Val Asp Gln Arg Glu Ile Glu Gln Leu Val Gly Asp Asp	
155 160 165	
ccc cag cgc tgc gcc tac ttc gag atc tcg gcc aag aag aac agc agc	702
Pro Gln Arg Cys Ala Tyr Phe Glu Ile Ser Ala Lys Lys Asn Ser Ser	
170 175 180	
ctg gac cag atg ttc cgc gcg ctc ttc gcc atg gcc aag ctg ccc agc	750
Leu Asp Gln Met Phe Arg Ala Leu Phe Ala Met Ala Lys Leu Pro Ser	
185 190 195	
gag atg agc cca gac ctg cac cgc aag gtc tcg gtg cag tac tgc gac	798
Glu Met Ser Pro Asp Leu His Arg Lys Val Ser Val Gln Tyr Cys Asp	
200 205 210 215	
gtg ctg cac aag aag gcg ctg cgg aac aag aag ctg ctg cgg gcc ggc	846
Val Leu His Lys Lys Ala Leu Arg Asn Lys Lys Leu Leu Arg Ala Gly	
220 225 230	
agc ggc ggc ggc ggc ggc gac ccg ggc gac gcc ttt ggc atc gtg gca	894
Ser Gly Gly Gly Gly Gly Asp Pro Gly Asp Ala Phe Gly Ile Val Ala	
235 240 245	
ccc ttc gcg cgc cgg ccc agc gta cac agc gac ctc atg tac atc cgc	942
Pro Phe Ala Arg Arg Pro Ser Val His Ser Asp Leu Met Tyr Ile Arg	
250 255 260	

gag aag gcc agc gcc ggc agc cag gcc aag gac aag gag cgc tgc gtc 990
 Glu Lys Ala Ser Ala Gly Ser Gln Ala Lys Asp Lys Glu Arg Cys Val
 265 270 275
 atc agc taggagcccc gccgcgctgg cgacacaacc taaggaggac ctttttgtta 1046
 Ile Ser
 280
 agtcaaatcc aacggccccg tgcgccccag gccgggagcg cgcgcggact ggcgtctccc 1106
 ctcccggcga tccgccccca gcactgggga ggcgccactg aaccgagaag ggacgggtcat 1166
 ctgctccgga aggaaagaga acgggccaag actgggacta ttccccaccc ccgggtcccc 1226
 attgaggccc gccacccccca taactttggg agcgagggcc cagccgaggg tggattttatc 1286
 ttctcaaaga cctaagagtg agcgcgggggt gggggaggga tgtgaagtta tccagcctct 1346
 gctaggcttc aagaaaccgt catgccccgt tgagggtcag gacccacggg gcattatctt 1406
 gtctgtgatt ccgggttgct gtgacagccg gtagagcctc tgccctcccg aaactaagcg 1466
 ggggggctg ggtcaaatca tagccaagtg acttgtttac atgtgagtga aactgcacaa 1526
 aggaacacaa aacaaaactt gcactttaac ggtagttccg gtgtcaacat ggacacgaac 1586
 aaaaccttac ccaggtgttt atactgtgtg tgtgtgaggt ctttaaagtt attgctttat 1646
 ttgggttttt aatatacaat aaaataattt aaaatggaaa aaaaaaaaaa aaaaaaaaaa 1706
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagcggccgc tcgagcatgc 1766
 atctagaggg ccgcatcatg taattagtta tgaac 1801

<210> 4

<211> 281

<212> PRT

<213> Homo Sapien

<400> 4

Met Lys Leu Ala Ala Met Ile Lys Lys Met Cys Pro Ser Asp Ser Glu
 1 5 10 15

Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
 20 25 30

Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
 35 40 45

Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
 50 55 60

Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
65 70 75 80

Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
145 150 155 160

Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly
225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
245 250 255

Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
260 265 270

Lys Asp Lys Glu Arg Cys Val Ile Ser
275 280

<210> 5

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 5

ctgctggtcg acgcggccgc tcatataata ccaatttttt taaggttttg ctgg

54

<210> 6

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 6

gtttgatgtg ggtgctcagc ggtctgag

28

<210> 7

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 7

ctcagaaccg ctgagcaccc acatcaaac

29

<210> 8

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 8
cgggatccat gaaactggcc gcgatgatca agaag

35

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 9
ggaattccta gctgatgacg cagcgctc

28

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 10
ggatccatgc aaacgctaaa gtgtg

25

<210> 11

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 11
gaattcgact acaaaattgc acatttttta c

31

<210> 12

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 12

cgcatggtca tcctcgtttc gtccaaggtg g

31

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 13

ccaccttgga cgaaacgagg atgaccatgc g

31

<210> 14

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 14

gctcgccaa ggtgggtaag acggccatcg tgtcg

35

<210> 15

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 15

cgacacgatg gccgtcttaa ccaccttgga cgagc

35

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 16

cctcgacacg tccgctaacc acccggtccc cg

32

<210> 17

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 17

cggggaacgg gtggttagcg gacgtgtcga gg

32

<210> 18

<211> 8

<212> PRT

<213> Unknown

<220>

<223> The phosphate/magnesium binding region GXXXXGK(S/T)

<220>

<221> MISC_FEATURE

<222> (2) .. (5)

<223> Xaa's at positions 2-5 may be any amino acid.

<220>

<221> MISC_FEATURE

<222> (8) .. (8)

<223> Xaa at position 8 may be Serine or Threonine acid.

<400> 18

Gly Xaa Xaa Xaa Xaa Gly Lys Xaa
1 5

<210> 19

<211> 4

<212> PRT

<213> Unknown

<220>

<223> The phosphate/magnesium binding region DXXG

<220>

<221> MISC_FEATURE

<222> (2) .. (3)

<223> Xaa's at positions 2,3 may be any amino acid.

<400> 19

Asp Xaa Xaa Gly
1

<210> 20

<211> 4

<212> PRT

<213> Unknown

<220>

<223> The guanine base binding loop NKXD

<220>

<221> MISC_FEATURE

<222> (3) .. (3)

<223> Xaa at position 3 may be any amino acid.

<400> 20

Asn Lys Xaa Asp

1

<210> 21

<211> 5

<212> PRT

<213> Unknown

<220>

<223> The guanine base binding lopp EXSAK

<220>

<221> MISC_FEATURE

<222> (2) .. (2)

<223> Xaa at position 2 may be any amino acid

<400> 21

Glu Xaa Ser Ala Lys

1

5

<210> 22

<211> 4

<212> PRT

<213> Unknown

<220>

<223> The C-terminal CAAX.

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Xaa at position 2 or 3 may be any aliphatic amino acid residue

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 may be any amino acid

<400> 22

Cys Xaa Xaa Xaa

1

<210> 23

<211> 7

<212> PRT

<213> Homo Sapiens

<400> 23

Gln Ala Lys Asp Lys Glu Arg

1

5

<210> 24

<211> 1691

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (45)..(587)

<223>

<400> 24

taagaagttg tacttaaagc ggaggagcta agccacctgc caaa atg tgc aaa gga 56
Met Cys Lys Gly
1

ctt gca gct ttg ccc cac tca tgc ctg gaa agg gcc aag gag att aag 104
Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala Lys Glu Ile Lys
5 10 15 20

atc aag ttg gga att ctc ctc cag aag cca gac tca gtt ggt gac ctt 152
Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser Val Gly Asp Leu
25 30 35

gtc att ccg tac aat gag aag cca gag aaa cca gcc aag acc cag aaa 200
Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala Lys Thr Gln Lys
40 45 50

acc tcg ctg gac gag gcc ctg cag tgg cgt gat tcc ctg gac aaa ctc 248
Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser Leu Asp Lys Leu
55 60 65

ctg cag aac aac tat gga ctt gcc agt ttc aaa agt ttc ctg aag tct 296
Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser Phe Leu Lys Ser
70 75 80

gaa ttc agt gag gaa aac ctt gag ttc tgg att gcc tgt gag gat tac 344
Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala Cys Glu Asp Tyr
85 90 95 100

aag aag atc aag tcc cct gcc aag atg gct gag aag gca aag caa att 392
Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys Ala Lys Gln Ile
105 110 115

tat gaa gaa ttc att caa acg gag gct cct aaa gag gtg aat att gac 440
Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu Val Asn Ile Asp
120 125 130

cac ttc act aag gac atc aca atg aag aac ctg gtg gaa cct tcc ctg 488
His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val Glu Pro Ser Leu
135 140 145

agc agc ttt gac atg gcc cag aaa aga atc cat gcc ctg atg gaa aag 536
Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala Leu Met Glu Lys
150 155 160

gat tct ctg cct cgc ttt gtg cgc tct gag ttt tat cag gag tta atc 584
Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr Gln Glu Leu Ile
165 170 175 180

aag tagtaattta gccaggctat gaaatcatcc tgtgagttat ttcctccata 637
Lys

ataaccctgc atttccatt aatctacata tcttcccaca gcagctttgc tcagtgatac 697

ccacatggga aaaatcccag gggatgttgc ttactctttt tgcccacact gctttggata 757

cttatctact gtccgaaggc cttctttccc cactcaattc ttcctgccct gttattaatt 817

aagatatctt cagcttgtag tcagacccaa tcagaatcac agaaaaatcc tgcctaaggc 877

aaagaaatat aagacaagac tatgatataca atgaatgtgg gttaagtaat agatttccag 937

ctaaattggt ctaaaaaaga atattaagtg tggacagacc tatttcaaag gagcttaatt 997
 gatctcactt gttttagttc tgatccaggg agatcacccc tctaattatt tctgaacttg 1057
 gtttaataaaa gtttataaga tttttatgaa gcagccactg tatgatattt taagcaaata 1117
 tgttatttaa aatattgatc cttcccttgg accaccttca tgttagttgg gtattataaa 1177
 taagagatac aaccatgaat atattatggt tatacaaaat caatctgaac acaattcata 1237
 aagattttctc ttttatacct tcctcactgg cccctccac ctgcccatag tcaccaaatt 1297
 ctgttttaaa tcaatgacct aagatcaaca atgaagtatt ttataaatgt atttatgctg 1357
 ctagactgtg ggtcaaagt ttccattttc aaattattta gaattcttat gagtttaaaa 1417
 tttgtaaatt tctaaatcca atcatgtaa atgaaactgt tgctccattg gagtagtctc 1477
 ccacctaagt atcaagatgg ctatatgcta aaaagagaaa atatggtcaa gtctaaaatg 1537
 gctaattgtc ctatgatgct attatcatag actaatgaca tttatcttca aaacacaaaa 1597
 ttgtctttag aaaaattaat gtgattacag gtagaggcct tctaggtgag acacttttaa 1657
 ggtacactgc attttgcaaa aaaaaaaaaa aaaa 1691

<210> 25

<211> 181

<212> PRT

<213> Homo Sapiens

<400> 25

Met Cys Lys Gly Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala
 1 5 10 15

Lys Glu Ile Lys Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser
 20 25 30

Val Gly Asp Leu Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala
 35 40 45

Lys Thr Gln Lys Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser
 50 55 60

Leu Asp Lys Leu Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser
 65 70 75 80

Phe Leu Lys Ser Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala
 85 90 95

Cys Glu Asp Tyr Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys
100 105 110

Ala Lys Gln Ile Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu
115 120 125

Val Asn Ile Asp His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val
130 135 140

Glu Pro Ser Leu Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala
145 150 155 160

Leu Met Glu Lys Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr
165 170 175

Gln Glu Leu Ile Lys
180

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 26
ccagatctaa agatgccgat ttgggcg

27

<210> 27

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 27
ccccatgggtt ttatatattgt tgtaaaaagt ag

32

<210> 28

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 28

cgggatccat gtgcaaaggg cttgcaggtc

30

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 29

ccgctcgagt taggcacact gagggacc

28

<210> 30

<211> 41

<212> DNA

<213> Homo Sapiens

<400> 30

agtcggtacc cgcatagatc tgcaggatgc cctttttgac g

41

<210> 31

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 31
gtacgtcgac tttgattttc agaaacttga tggc 34

<210> 32

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 32
tggcctcgag atgacaaatt caaaagaaga cg 32

<210> 33

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 33
atcactgcag ctatgctaca acattccaaa at 32

<210> 34

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 34
gggtcatgaa actggccgcg atgatcaaga ag 32

<210> 35

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 35

gatagtcgac ctagctgatg acgcagcgct c

31

<210> 36

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 36

cgcatggtca tctctgtttc gtccaagggtg g

31

<210> 37

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 37

ccaccttgga cgaaacgagg atgaccatgc g

31

<210> 38

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 38

ccaaggacaa ggagcgcagc gtcacagct ag

32

<210> 39

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 39

ctagctgatg acgctgcgct ccttgctcctt gg

32

<210> 40

<211> 837

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (1)..(834)

<223>

<400> 40

atg cct gct tct ctc gct ttg ttg cag ccc cga gcc atg atg aag act
Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr
1 5 10 15

48

ttg tcc agc ggg aac tgc acg ctc agt gtg ccc gcc aaa aac tca tac
Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala Lys Asn Ser Tyr
20 25 30

96

cgc atg gtg gtg ctg ggt gcc tct cgg gtg ggc aag agc tcc atc gtg
Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val
35 40 45

144

tct cgc ttc ctc aat ggc cgc ttt gag gac cag tac aca ccc acc atc
Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile
50 55 60

192

gag gac ttc cac cgt aag gta tac aac atc cgc ggc gac atg tac cag	240
Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln	
65 70 75 80	
ctc gac atc ctg gat acc tct ggc aac cac ccc ttc ccc gcc atg cgc	288
Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg	
85 90 95	
agg ctg tcc atc ctc aca ggg gat gtc ttc atc ctg gtg ttc agc ctg	336
Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu	
100 105 110	
gat aac cgg gag tcc ttc gat gag gtc aag cgc ctt cag aag cag atc	384
Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile	
115 120 125	
ctg gag gtc aag tcc tgc ctg aag aac aag acc aag gag gcg gcg gag	432
Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu	
130 135 140	
ctg ccc atg gtc atc tgt ggc aac aag aac gac cac ggc gag ctg tgc	480
Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys	
145 150 155 160	
cgc cag gtg ccc acc acc gag gcc gag ctg ctg gtg tcg ggc gac gag	528
Arg Gln Val Pro Thr Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu	
165 170 175	
aac tgc gcc tac ttc gag gtg tcg gcc aag aag aac acc aac gtg gac	576
Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp	
180 185 190	
gag atg ttc tac gtg ctc ttc agc atg gcc aag ctg cca cac gag atg	624
Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met	
195 200 205	
agc ccc gcc ctg cat cgc aag atc tcc gtg cag tac ggt gac gcc ttc	672
Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe	
210 215 220	
cac ccc agg ccc ttc tgc atg cgc cgc gtc aag gag atg gac gcc tat	720
His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr	
225 230 235 240	
ggc atg gtc tcg ccc ttc gcc cgc cgc ccc agc gtc aac agt gac ctc	768
Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu	
245 250 255	
aag tac atc aag gcc aag gtc ctt cgg gaa ggc cag gcc cgt gag agg	816
Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg	
260 265 270	
gac aag tgc acc atc cag tga	837
Asp Lys Cys Thr Ile Gln	
275	

<210> 41

<211> 278

<212> PRT

<213> Homo Sapiens

<400> 41

Met	Pro	Ala	Ser	Leu	Ala	Leu	Leu	Gln	Pro	Arg	Ala	Met	Met	Lys	Thr
1				5				10						15	
Leu	Ser	Ser	Gly	Asn	Cys	Thr	Leu	Ser	Val	Pro	Ala	Lys	Asn	Ser	Tyr
			20					25					30		
Arg	Met	Val	Val	Leu	Gly	Ala	Ser	Arg	Val	Gly	Lys	Ser	Ser	Ile	Val
		35					40					45			
Ser	Arg	Phe	Leu	Asn	Gly	Arg	Phe	Glu	Asp	Gln	Tyr	Thr	Pro	Thr	Ile
	50					55					60				
Glu	Asp	Phe	His	Arg	Lys	Val	Tyr	Asn	Ile	Arg	Gly	Asp	Met	Tyr	Gln
65					70					75					80
Leu	Asp	Ile	Leu	Asp	Thr	Ser	Gly	Asn	His	Pro	Phe	Pro	Ala	Met	Arg
			85						90					95	
Arg	Leu	Ser	Ile	Leu	Thr	Gly	Asp	Val	Phe	Ile	Leu	Val	Phe	Ser	Leu
			100					105					110		
Asp	Asn	Arg	Glu	Ser	Phe	Asp	Glu	Val	Lys	Arg	Leu	Gln	Lys	Gln	Ile
		115					120					125			
Leu	Glu	Val	Lys	Ser	Cys	Leu	Lys	Asn	Lys	Thr	Lys	Glu	Ala	Ala	Glu
	130					135					140				
Leu	Pro	Met	Val	Ile	Cys	Gly	Asn	Lys	Asn	Asp	His	Gly	Glu	Leu	Cys
145					150					155					160
Arg	Gln	Val	Pro	Thr	Thr	Glu	Ala	Glu	Leu	Leu	Val	Ser	Gly	Asp	Glu
				165					170					175	
Asn	Cys	Ala	Tyr	Phe	Glu	Val	Ser	Ala	Lys	Lys	Asn	Thr	Asn	Val	Asp
			180					185					190		
Glu	Met	Phe	Tyr	Val	Leu	Phe	Ser	Met	Ala	Lys	Leu	Pro	His	Glu	Met
		195					200					205			

Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe
210 215 220

His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr
225 230 235 240

Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu
245 250 255

Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg
260 265 270

Asp Lys Cys Thr Ile Gln
275

<210> 42

<211> 15

<212> PRT

<213> Homo Sapiens

<400> 42

Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn Val Asp
1 5 10 15

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 43
ttctcgcgga tgtacatga

19

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 44

tccaccgcaa gttctactcc

20

<210> 45

<211> 1740

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (146)..(988)

<223>

<400> 45

gagcggagcc ggagcccca gcccagagccg cgcccagccc gagcagagcc ctccagccgc 60

tcaccccgcg tgccaccca ggcacctca gccgtctct gcccttctct cggccccgcg 120

cccgccctcg cggccccctct gccca atg aaa ctg gcc gcg atg atc aag aag 172

Met Lys Leu Ala Ala Met Ile Lys Lys
1 5

atg tgc ccg agc gac tcg gag ctg agt atc ccg gcc aag aac tgc tat 220

Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn Cys Tyr
10 15 20 25

cgc atg gtc atc ctc ggc tcg tcc aag gtg ggc aag acg gcc atc gtg 268

Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala Ile Val
30 35 40

tcg cgc ttc ctc acc ggc cgc ttc gag gac gcc tac acg cct acc atc 316

Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Pro Thr Ile
45 50 55

gag gac ttc cac cgc aag ttc tac tcc atc cgc ggc gag gtc tac cag 364

Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val Tyr Gln
60 65 70

ctc gac atc ctc gac acg tcc ggc aac cac ccg ttc ccc gcc atg cgg 412

Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg
75 80 85

cgc ctc tcc atc ctc aca gga gac gtt ttc atc ctg gtg ttc agt ctg	460
Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu	
90 95 100 105	
gac aac cgc gac tcc ttc gag gag gtg cag cgg ctc agg cag cag atc	508
Asp Asn Arg Asp Ser Phe Glu Glu Val Gln Arg Leu Arg Gln Gln Ile	
110 115 120	
ctc gac acc aag tct tgc ctc aag aac aaa acc aag gag aac gtg gac	556
Leu Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn Val Asp	
125 130 135	
gtg ccc ctg gtc atc tgc ggc aac aag ggt gac cgc gac ttc tac cgc	604
Val Pro Leu Val Ile Cys Gly Asn Lys Gly Asp Arg Asp Phe Tyr Arg	
140 145 150	
gag gtg gac cag cgc gag atc gag cag ctg gtg ggc gac gac ccc cag	652
Glu Val Asp Gln Arg Glu Ile Glu Gln Leu Val Gly Asp Asp Pro Gln	
155 160 165	
cgc tgc gcc tac ttc gag atc tcg gcc aag aag aac agc agc ctg gac	700
Arg Cys Ala Tyr Phe Glu Ile Ser Ala Lys Lys Asn Ser Ser Leu Asp	
170 175 180 185	
cag atg ttc cgc gcg ctc ttc gcc atg gcc aag ctg ccc agc gag atg	748
Gln Met Phe Arg Ala Leu Phe Ala Met Ala Lys Leu Pro Ser Glu Met	
190 195 200	
agc cca gac ctg cac cgc aag gtc tcg gtg cag tac tgc gac gtg ctg	796
Ser Pro Asp Leu His Arg Lys Val Ser Val Gln Tyr Cys Asp Val Leu	
205 210 215	
cac aag aag gcg ctg cgc aac aag aag ctg ctg cgg gcc ggc agc ggc	844
His Lys Lys Ala Leu Arg Asn Lys Lys Leu Leu Arg Ala Gly Ser Gly	
220 225 230	
ggc ggc ggc ggc gac ccg ggc gac gcc ttt ggc atc gtg gca ccc ttc	892
Gly Gly Gly Gly Asp Pro Gly Asp Ala Phe Gly Ile Val Ala Pro Phe	
235 240 245	
gcg cgc cgg ccc agc gta cac agc gac ctc atg tac atc cgc gag aag	940
Ala Arg Arg Pro Ser Val His Ser Asp Leu Met Tyr Ile Arg Glu Lys	
250 255 260 265	
gcc agc gcc ggc agc cag gcc aag gac aag gag cgc tgc gtc atc agc	988
Ala Ser Ala Gly Ser Gln Ala Lys Asp Lys Glu Arg Cys Val Ile Ser	
270 275 280	
taggagcccc gccgcgctgg cgacacaacc taaggaggac ctttttggtta agtcaaattcc	1048
aacggccccgg tgcgccccag gccgggagcg cgcgcggact ggcgtctccc ctccccggcga	1108
tccgccccca gcaactgggga ggcgccactg aaccgagaag ggacggtcat ctgctccgga	1168
aggaaagaga acgggccaag actgggacta ttccccaccc ccggtcccc attgaggccc	1228
gccacccccca taactttggg agcgagggcc cagccgaggg tggatttatc ttctcaaaga	1288
cctaagagtg agcgcggggg gggggaggga tgtgaagtta tccagcctct gctaggcttc	1348

aagaaaccgt catgcccgtg tgagggtcag gacccacggg gcattatctt gtctgtgatt 1408
ccgggttgct gtgacagccg gtagagcctc tgcctcccg aaactaagcg ggggggcgtg 1468
ggtcaaatca tagccaagtg acttgtttac atgtgagtga aactgcacaa aggaacacaa 1528
aacaaaactt gcactttaac ggtagttccg gtgtcaacat ggacacgaac aaaaccttac 1588
ccaggtgttt atactgtgtg tgtgtgaggt ctttaaagtt attgctttat ttgggttttt 1648
aatatacaat aaaataattt aaaatggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1708
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1740

<210> 46

<211> 281

<212> PRT

<213> Homo Sapiens

<400> 46

Met Lys Leu Ala Ala Met Ile Lys Lys Met Cys Pro Ser Asp Ser Glu
1 5 10 15

Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
20 25 30

Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
35 40 45

Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
50 55 60

Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
65 70 75 80

Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
 145 150 155 160

Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
 165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
 180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
 195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
 210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly
 225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
 245 250 255

Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
 260 265 270

Lys Asp Lys Glu Arg Cys Val Ile Ser
 275 280

<210> 47

<211> 189

<212> PRT

<213> Homo Sapiens

<400> 47

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
 1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
 20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
 35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
 50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
180 185

<210> 48

<211> 206

<212> PRT

<213> Homo Sapiens

<400> 48

Met Ala Ala Asn Lys Pro Lys Gly Gln Asn Ser Leu Ala Leu His Lys
1 5 10 15

Val Ile Met Val Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Leu
20 25 30

Gln Phe Met Tyr Asp Glu Phe Val Glu Asp Tyr Glu Pro Thr Lys Ala
35 40 45

Asp Ser Tyr Arg Lys Lys Val Val Leu Asp Gly Glu Glu Val Gln Ile
50 55 60

Asp Ile Leu Asp Thr Ala Gly Gln Glu Asp Tyr Ala Ala Ile Arg Asp
65 70 75 80

Asn Tyr Phe Arg Ser Gly Glu Gly Phe Leu Cys Val Phe Ser Ile Thr
85 90 95

Glu Met Glu Ser Phe Ala Ala Thr Ala Asp Phe Arg Glu Gln Ile Leu
100 105 110

Arg Val Lys Glu Asp Glu Asn Val Pro Phe Leu Leu Val Gly Asn Lys
115 120 125

Ser Asp Leu Glu Asp Lys Arg Gln Val Ser Val Glu Glu Ala Lys Asn
130 135 140

Arg Ala Glu Gln Trp Asn Val Asn Tyr Val Glu Thr Ser Ala Lys Thr
145 150 155 160

Arg Ala Asn Val Asp Lys Val Phe Phe Asp Leu Met Arg Glu Ile Arg
165 170 175

Ala Arg Lys Met Glu Asp Ser Lys Glu Lys Asn Gly Lys Lys Lys Arg
180 185 190

Lys Ser Leu Ala Lys Arg Ile Arg Glu Arg Cys Cys Ile Leu
195 200 205

<210> 49

<211> 205

<212> PRT

<213> Homo Sapiens

<400> 49

Met Ser Ser Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu
1 5 10 15

Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala
20 25 30

Asp Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe
35 40 45

Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys Leu Gln Ile
 50 55 60

Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr
 65 70 75 80

Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln
 85 90 95

Glu Ser Phe Asn Asn Val Lys Gln Trp Leu Gln Glu Ile Asp Arg Tyr
 100 105 110

Ala Ser Glu Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu
 115 120 125

Thr Thr Lys Lys Val Val Asp Tyr Thr Thr Ala Lys Glu Phe Ala Asp
 130 135 140

Ser Leu Gly Ile Pro Phe Leu Glu Thr Ser Ala Lys Asn Ala Thr Asn
 145 150 155 160

Val Glu Gln Ser Phe Met Thr Met Ala Ala Glu Ile Lys Lys Arg Met
 165 170 175

Gly Pro Gly Ala Thr Ala Gly Gly Ala Glu Lys Ser Asn Val Lys Ile
 180 185 190

Gln Ser Thr Pro Val Lys Gln Ala Gly Gly Gly Cys Cys
 195 200 205

<210> 50

<211> 210

<212> PRT

<213> Homo Sapiens

<400> 50

Met Thr Ala Ala Gln Ala Ala Gly Glu Glu Ala Pro Pro Gly Val Arg
 1 5 10 15

Ser Val Lys Val Val Leu Val Gly Asp Gly Gly Cys Gly Lys Thr Ser
 20 25 30

Leu Leu Met Val Phe Ala Asp Gly Ala Phe Pro Glu Ser Tyr Thr Pro
35 40 45

Thr Val Phe Glu Arg Tyr Met Val Asn Leu Gln Val Lys Gly Lys Pro
50 55 60

Val His Leu His Ile Trp Asp Thr Ala Gly Gln Asp Asp Tyr Asp Arg
65 70 75 80

Leu Arg Pro Leu Phe Tyr Pro Asp Ala Ser Val Leu Leu Leu Cys Phe
85 90 95

Asp Val Thr Ser Pro Asn Ser Phe Asp Asn Ile Phe Asn Arg Trp Tyr
100 105 110

Pro Glu Val Asn His Phe Cys Lys Lys Val Pro Ile Ile Val Val Gly
115 120 125

Cys Lys Thr Asp Leu Arg Lys Asp Lys Ser Leu Val Asn Lys Leu Arg
130 135 140

Arg Asn Gly Leu Glu Pro Val Thr Tyr His Arg Gly Gln Glu Met Ala
145 150 155 160

Arg Ser Val Gly Ala Val Ala Tyr Leu Glu Cys Ser Ala Arg Leu His
165 170 175

Asp Asn Val His Ala Val Phe Gln Glu Ala Ala Glu Val Ala Leu Ser
180 185 190

Ser Arg Gly Arg Asn Phe Trp Arg Arg Ile Thr Gln Gly Phe Cys Val
195 200 205

Val Thr
210

<210> 51

<211> 191

<212> PRT

<213> Homo Sapiens

<400> 51

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr
20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly
35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val
65 70 75 80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys
85 90 95

Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu
100 105 110

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys
115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys
130 135 140

Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu
145 150 155 160

Thr Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala
165 170 175

Leu Glu Pro Pro Glu Thr Gln Pro Lys Arg Lys Cys Cys Ile Phe
180 185 190

<210> 52

<211> 192

<212> PRT

<213> Homo Sapiens

<400> 52

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
 1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr
 20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Ser
 35 40 45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr
 50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile
 65 70 75 80

Cys Phe Ser Leu Val Ser Pro Ala Ser Tyr Glu Asn Val Arg Ala Lys
 85 90 95

Trp Phe Pro Glu Val Arg His His Cys Pro Ser Thr Pro Ile Ile Leu
 100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys
 115 120 125

Leu Lys Glu Lys Lys Leu Ala Pro Ile Thr Tyr Pro Gln Gly Leu Ala
 130 135 140

Leu Ala Lys Glu Ile Asp Ser Val Lys Tyr Leu Glu Cys Ser Ala Leu
 145 150 155 160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val
 165 170 175

Leu Cys Pro Gln Pro Thr Arg Gln Gln Lys Arg Ala Cys Ser Leu Leu
 180 185 190

<210> 53

<211> 181

<212> PRT

<213> Homo Sapiens

<400> 53

Met Gly Gly Phe Phe Ser Ser Ile Phe Ser Ser Leu Phe Gly Thr Arg
1 5 10 15

Glu Met Arg Ile Leu Ile Leu Gly Leu Asp Gly Ala Gly Lys Thr Thr
20 25 30

Ile Leu Tyr Arg Leu Gln Val Gly Glu Val Val Thr Thr Ile Pro Thr
35 40 45

Ile Gly Phe Asn Val Glu Thr Val Thr Tyr Lys Asn Leu Lys Phe Gln
50 55 60

Val Trp Asp Leu Gly Gly Gln Thr Ser Ile Arg Pro Tyr Trp Arg Cys
65 70 75 80

Tyr Tyr Ser Asn Thr Asp Ala Val Ile Tyr Val Val Asp Ser Cys Asp
85 90 95

Arg Asp Arg Ile Gly Ile Ser Lys Ser Glu Leu Val Ala Met Leu Glu
100 105 110

Glu Glu Glu Leu Arg Lys Ala Ile Leu Val Val Phe Ala Asn Lys Gln
115 120 125

Asp Met Glu Gln Ala Met Thr Ser Ser Glu Met Ala Asn Ser Leu Gly
130 135 140

Leu Pro Ala Leu Lys Asp Arg Lys Trp Gln Ile Phe Lys Thr Ser Ala
145 150 155 160

Thr Lys Gly Thr Gly Leu Asp Glu Ala Met Glu Trp Leu Val Glu Thr
165 170 175

Leu Lys Ser Arg Gln
180

<210> 54

<211> 229

<212> PRT

<213> Homo Sapiens

<400> 54

Met Asp Pro Asn Gln Asn Val Lys Cys Lys Ile Val Val Val Gly Asp
1 5 10 15

Ser Gln Cys Gly Lys Thr Ala Leu Leu His Val Phe Ala Lys Asp Cys
20 25 30

Phe Pro Glu Asn Tyr Val Pro Thr Val Phe Glu Asn Tyr Thr Ala Ser
35 40 45

Phe Glu Ile Asp Thr Gln Arg Ile Glu Leu Ser Leu Trp Asp Thr Ser
50 55 60

Gly Ser Pro Tyr Tyr Asp Asn Val Arg Pro Leu Ser Tyr Pro Asp Ser
65 70 75 80

Asp Ala Val Leu Ile Cys Phe Asp Ile Ser Arg Pro Glu Thr Leu Asp
85 90 95

Ser Val Leu Lys Lys Trp Lys Gly Glu Ile Gln Glu Phe Cys Pro Asn
100 105 110

Thr Lys Met Leu Leu Val Gly Cys Lys Ser Asp Leu Arg Thr Asp Val
115 120 125

Ser Thr Leu Val Glu Leu Ser Asn His Arg Gln Thr Pro Val Ser Tyr
130 135 140

Asp Gln Gly Ala Asn Met Ala Lys Gln Ile Gly Ala Ala Thr Tyr Ile
145 150 155 160

Glu Cys Ser Ala Leu Gln Ser Glu Asn Ser Val Arg Asp Ile Phe His
165 170 175

Val Ala Thr Leu Ala Cys Val Asn Lys Thr Asn Lys Asn Val Lys Arg
180 185 190

Asn Lys Ser Gln Arg Ala Thr Lys Arg Ile Ser His Met Pro Ser Arg
195 200 205

Pro Glu Leu Ser Ala Val Ala Thr Asp Leu Arg Lys Asp Lys Ala Lys
210 215 220

Ser Cys Thr Val Met
225

<210> 55

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 55

Lys Ile Val Val Val Gly Asp Ser Gln Cys Gly Lys Thr Ala Leu Leu
1 5 10 15

<210> 56

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 56

Lys Ile Val Val Val Gly Asp Ala Glu Cys Gly Lys Thr Ala Leu Leu
1 5 10 15

<210> 57

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 57

Lys Leu Val Leu Val Gly Asp Val Gln Cys Gly Lys Thr Ala Met Leu
1 5 10 15

<210> 58

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 58

Lys Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu
1 5 10 15

<210> 59

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 59

Lys Leu Val Val Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu
1 5 10 15

<210> 60

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 60

Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu
1 5 10 15

<210> 61

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 61

Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu
1 5 10 15

<210> 62

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 62

Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys Ser Ala Leu Thr
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 63

Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala Ile Val
1 5 10 15

<210> 64

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 64

Leu Ser Leu Trp Asp Thr Ser Gly Ser Pro Tyr Tyr Asp
1 5 10

<210> 65

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 65

Leu Asn Met Trp Asp Thr Ser Gly Ser Ser Tyr Tyr Asp
1 5 10

<210> 66

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 66

Leu Ser Leu Trp Asp Thr Ser Gly Ser Pro Tyr Tyr Asp
1 5 10

<210> 67

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 67

Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp
1 5 10

<210> 68

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 68

Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp
1 5 10

<210> 69

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 69

Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr Asp
1 5 10

<210> 70

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 70

Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp
1 5 10

<210> 71

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 71

Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr Asp
1 5 10

<210> 72

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 72

Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro
1 5 10

<210> 73

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Probe/Primer

<400> 73
ctcatggagc tcaaactggt actattaggt gccg

34